

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 20, 2003, 06:52:11 ; Search time 1 Seconds
(without alignments)
0.436 Million cell updates/sec

-228-3

Title: us-09-854-280-3

Perfect score: 1073

Sequence: 1 MTLPLGLFLTLWLTCLAH.....FHTEFIHPVGCTCVLPSPV 197

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 1107 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=soft -Q=us-09-854-280-3 -DB=us-09-480-297a-22
-SUFFIX=ptc -OUT=align_3_22 -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPG=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-09-480-297a-22:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	1107	1	us-09-480-297a-22

ALIGNMENTS

RESULT 1
us-09-480-297a-22

Alignment Scores:

Pred. No.: 0 Length: 1107
Score: 1073.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

us-09-854-280-3 (1-197) x us-09-480-297a-22 (1-1107)

Qy 1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
Db 115 ATGACGCTCTCCCGGCTCTCTGTTCTGACCTGGCTGCACACATGCTGGCCACCAT 174

Qy 21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
Db 175 GACCCCTCCCTCAGGGGACCCCCACAGTACCGGTACCCACACTGCTACTCGGCTAG 234
Qy 41 GluLeuProLeuGlyGlnAlaProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
Db 235 GAACCTGCCCTCGGCCAGGCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGAG 294
Qy 61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
Db 295 GCTTGGCTGTAGCCCTGGTGTCCAGCTGGAGGACGACCAAGCCACAGGGGAGGCACGAG 354
Qy 81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
Db 355 AGGCCCTCAGCTACGACCCAGTCCCGGTGCTGGCCGGAGGAGGTGTTGGAGGCAC 414
Qy 101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
Db 415 ACCCACCAGCGCTCCATCTCACCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 474
Qy 121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
Db 475 CCACAGAGCTGGCCTTCCCGAGTGGCTGTGCAGAGGCTGTATCGATGCACGACGGGC 534
Qy 141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuValLeuArgArg 160
Db 535 CGCGAGACAGCTGGCTCACTCCGCGGCTGCTCCAGAGCCCTGCTGCTGCTGGCCGCG 594
Qy 161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
Db 595 CGGCCCTGCTCCCGACGCGCTCGGGGCTCCCCACACCTGGGGGCTTTGCTTCCACACC 654
Qy 181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
Db 655 GAGTTCATCCACGTCGCCGCTCGGCTGCACCTGCGTGTGCTGCCCGCTTCAGTG 705

Search completed: May 20, 2003, 06:52:12
Job time : 1 secs